

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 10:52:07 ; Search time 2658.23 seconds
(without alignments)
4226.338 Million cell updates/sec

Title: US-09-602-833a-3

Perfect score: 681

Sequence: 1 atcagaattcgtgatcgtcc.....ctttagcctcaatttga 681

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_om: *
20: em_ov: *
21: em_or: *
22: em_pat: *
23: em_ph: *
24: em_pl: *
25: em_ro: *
26: em_sts: *
27: em_sy: *
28: em_un: *
29: em_vl: *
30: em_htgo_hum: *
31: em_htgo_inv: *
32: em_htgo_rod: *
33: em_htg_hum: *
34: em_htg_inv: *
35: em_htg_rod: *
36: em_htg_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8 SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	681	100.0	681	6 AX063234	AX063234 Sequence
2	681	100.0	1116	6 AX063232	AX063232 Sequence
3	681	100.0	4860	9 HSA308569	AJ308569 Homo sapi
4	392.8	57.7	172966	9 AC013467	AC013467 Homo sapi
5	161	23.6	145795	2 HSA310966	AJ310966 Homo sapi
6	161	23.6	202324	2 AC068720	AC068720 Homo sapi
7	137.8	20.2	202324	2 AC068720	AC068720 Homo sapi
8	130.4	19.1	2056	9 AK021919	AK021919 Homo sapi
9	60.8	8.9	1658	9 AF359380	AF359380 Homo sapi
10	60.8	8.9	2156	9 BC003193	BC003193 Homo sapi
11	59.8	8.9	2886	9 AF332199	AF332199 Homo sapi
12	59.8	8.8	216481	2 AC027653	AC027653 Mus muscu
13	58.2	8.5	133841	2 AC079990	AC079990 Rattus no
14	58.2	8.5	188150	2 AC079378	AC079378 Rattus no
15	57.4	8.4	1127	9 AY007147	AY007147 Homo sapi
16	57.4	8.4	2384	6 AX099399	AX099399 Sequence
17	57.4	8.4	162598	2 AC079091	AC079091 Homo sapi
18	57.4	8.4	174297	2 AL512367	AL512367 Homo sapi
19	57.4	8.4	212127	2 AL391497	AL391497 Homo sapi
20	56.8	8.3	182366	2 AC041041	AC041041 Homo sapi
21	56.8	8.3	182885	2 AC087763	AC087763 Homo sapi
22	56.8	8.3	182914	2 AC090567	AC090567 Homo sapi
23	56.8	8.3	185510	2 AC011018	AC011018 Homo sapi
24	55.8	8.2	2410	9 AK001332	AK001332 Homo sapi
25	55.2	8.1	3159	9 AB016816	AB016816 Homo sapi
26	55.2	8.1	6125	6 AX188327	AX188327 Sequence
27	54.4	8.0	142296	2 AF004035	AF004035 Homo sapi
28	54.4	8.0	142396	2 HSAC000120	AC000120 Human BAC
29	54.4	8.0	169580	2 AC092762	AC092762 Pan trogl
30	54.4	8.0	257967	2 AL365337	AL365337 Mus muscu
31	52.8	7.8	4635	3 DME271647	AJ271647 Drosophill
32	52.8	7.8	5988	3 AF190774	AF190774 Drosophill
33	52.8	7.8	7166	3 DME232084	AJ252084 Drosophill
34	52.6	7.7	2893	3 BC009239	BC009239 Homo sapi
35	52.6	7.7	118533	2 AC020205	AC020205 Drosophill
36	52.6	7.7	165852	2 AC092874	AC092874 Sus scrofa
37	52.6	7.7	173970	3 AC005286	AC005286 Drosophill
38	52.6	7.7	263693	3 AE003793	AE003793 Drosophill
39	51.4	7.5	8373	8 AF290191	AF290191 Cryptococ
40	51.2	7.5	156294	2 AC092409	AC092409 Papilio cyn
41	51.2	7.5	198746	2 AC092517	AC092517 Papilio cyn
42	51	7.5	6248	9 D86984	D86984 Human mRNA
43	50.4	7.4	2620	9 AK001637	AK001637 Homo sapi
44	50.4	7.4	2754	9 BC003407	BC003407 Homo sapi
45	50.4	7.4	2846	9 BC008586	BC008586 Homo sapi

ALIGNMENTS

RESULT 1
AX063234 LOCUS AX063234 681 bp DNA
DEFINITION Sequence 3 from Patent WO0070959.
ACCESSION AX063234
VERSION AX063234.1 GI:12541060
KEYWORDS
SOURCE
ORGANISM human.

ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 681)
Turner,A.C., Zambrowicz,B., Nehls,M., Friedrich,G.A. and Sands,A.T.
Human genes and proteins encoded thereby
Patent: WO 0078959-A 3 28-DEC-2000;

JOURNAL

Lexicon Genetics Incorporated (US)
Location/Qualifiers
1. .681
source

/organism="Homo sapiens"
/db_xref="taxon:9606"

QY 601 aaagccatattgaagaccttaagaagaagatcgttccagctataccaccaagtg 660
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Db 1036 AAAGCCTATATTGAAGACCTTAAGAAGAAAGAAATCTGTCCAGCTATACACCAAGTG 1095
QY 661 tcttttagccttcaacttga 681
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Db 1096 TCTTTAGCCTTCAACTTTGA 1116
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RESULT 3
HSA308569 4860 bp mRNA PRI 06-JUN-2001
LOCUS Homo sapiens mRNA for leucine-rich repeat-containing 2 protein
DEFINITION (LRRC2 gene).
ACCESSION AJ308569
VERSION AJ308569.2 GI:14330408
KEYWORDS leucine-rich repeat-containing 2 protein; LRRC2 gene.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4860)
AUTHORS Kiss, H., Yang, Y., Kost-Alimova, M., Szeles, A., Kholodnyuk, I.,
Kedra, D., Kiss, C., Klein, G., Imreh, S. and Dunamski, J. P.
TITLE Transcriptional map of the Common Eliminated Region 1 on human
3p21.3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4860)
AUTHORS Kiss, H.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
REMARK Revised by [3]
REFERENCE 3 (bases 1 to 4860)
AUTHORS Kiss, H.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
COMMENT On Jun 8, 2001 this sequence version replaced gi:13186111.
FEATURES
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Location/Qualifiers
1..4860
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/db_xref="taxon:9606"
/chromosome="3"
/map="3p21.3"
168..1283
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168..1283
/gene="LRRC2"
/codon_start=1
/product="leucine-rich repeat-containing 2 protein"
/protein_id="CAC3442.1"
/db_xref="GI:13186112"
/translation="MGKVVVFDISVIALMETRVKKHKMOKKEVERLEKSALEKIK
EENFVAECRRKGIPOAVYCKNGFIDTSVALLKIRBNITROSSIPKDGKSSAFV
FELSGHMEIPDSLIKQOTLRMYISNTLIQIIPYIQIQFQMRITLDPKNOISHP
AETGCKLNKELVNGFNYLKSITPELDDCENLRDSCGNLELMELEFELSNLKQYTF
VDTSANKFSSVPICVSRMSNLQWLDISSNNLTJLPDIDIDLELQSLVLYKNKLTYP
YSMLNKKLTLLVSGDHLVLEPTALCDSSTPKPFVSIAMNPIDNAQCEDEGNEIMSE
RDRQHFDEVMKAYIEDIKERESVPSYTTKVSFSLQ"
BASE COUNT 1480 a 924 c 1162 g 1294 t
ORIGIN
Query Match 100.0%; Score 681; DB 9; Length 4860;
Best Local Similarity 100.0%; Pred. No. 4.8e-168;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atggaattcgtgacgtgcgcaaaaacaaatctccacatcttccagcagaatcgtgtg 60
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Db 603 ATGGAATTCGTGATCTGCCAAAAAACCAAAATCTACATCTTCCAGCAAGAAATCGTGTG 662
QY 61 ttgaagaacctgaagaactcaatgatggttcaactatctgaagacattcccgaa 120
|||||
Db 663 TTGAAGAACCCTGAANAAGCTCAATGTGGTTCAACTATCTGAAGAGATTCTCCGAA 722
QY 121 ttggagatgtgaaaactctagagagactgattgtctctgaaaactagaataatgag 180
|||||
Db 723 TTGGGAGATGTGAAAATCTAGAGAGACTGATGTCTCGAATCTAGATTAATGATGAG 782
QY 181 ctgcctttgaattaagaatttgaagaagttacattgtagatlatccagaacaag 240
Db 783 CTGCCCTTTGAATTAAGTAATTTGAAGCAAGTTACATTTGATGATATCTCAGCAAAAG 842
QY 241 ttccacagtcaccaactcgtgctcgtcgagatgctcgaatttgcagtggttgatatacg 300
Db 843 TTTTCAGATGCCAAATCTGTCCTCGGATGCGAATTTGACAGTGGTGGATATACG 902
QY 301 agcaataacctgaccgacctgcgcaagatatagacagcctagaagcctcagagctt 360
Db 903 AGCAATAACCTGACCGACCTGCCGCAATATAGACAGCTAGAGAGACTCAGAGCTTT 962
QY 361 ctcttgataaacaagaagttgacctaccctccattccatgctgaactgaagaagctc 420
Db 963 CTTTGTATATAAACAAGTTGACCTACCTTCCATTCCATGCTGAACCTGAAGAGCTC 1022
QY 421 actctgttagtcgacagtgaggacattgtgtgagctcccaactgccttgcactca 480
Db 1023 ACTCTGTAGTCGTCAGGGGGACCATTTGTGTGAGCTCCCACTGCCCTTTGTGATCA 1082
QY 481 tccacaccttaaaatctgtaagcctatagacaatccatattgataatgccaatgaa 540
Db 1083 TCCACACCTTAAATTTGTAGGCTTATGACATCTTATGTAATGCCCATGTGAA 1142
QY 541 gatggcaatgaataatgagaagtgaacggagatcgccaacatttgataaagaagtacg 600
Db 1143 GATGGCAATGAATAATGAGAAAGTGAACGGGATGCCCAACATTTGATTAAGAAGTATG 1202
QY 601 aaagccatattgaagaccttaagaagaagaatcttccagctataccaccaagtg 660
Db 1203 AAAGCCTATATTGAAGACCTTAAGAAGAAAGAAATCTGTCCAGCTATACCAAGAGTG 1262
QY 661 tcttttagccttcaacttga 681
Db 1263 TCTTTAGCCTTCAACTTTGA 1283
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RESULT 4
AC013467/c 172966 bp DNA PRI 25-MAY-2001
LOCUS Homo sapiens clone Rpl1-451F14, complete sequence.
AC013467
ACCESSION AC013467
VERSION AC013467.8 GI:14196420
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 172966)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 172966)
AUTHORS Waterston, R. H.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 3 (bases 1 to 172966)
AUTHORS Waterston, R. H.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA
 On May 25, 2001 this sequence version replaced gi:13624417.
 Center project name: H_NH0451P14.
 Location/Qualifiers
 source 1..172966
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="RP11-451P14"

BASE COUNT 57371 a 34327 c 31782 g 49486 t
 ORIGIN

Query Match 57.7% Score 392.8; DB 9; Length 172966;
 Best Local Similarity 88.8%; Pred. No. 3,2e+92;
 Matches 460; Conservative 0; Mismatches 52; Indels 6; Gaps 3;

QY 1 atgaattctgcatctcccaaaacccaatctcacatcttcagcagagaatcggtt 60
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 Db 168926 ATGAGAAATTCAGATCTCCCAAGAAACAAATCTCACATTTCCAGCTRAACTCAGTTGT 168867

QY 61 ttgaagaacctgaaagaaactcaatgttggttcaactatctgaagaagcatctccacagaa 120
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 Db 168866 TTGAAGAACCTGAATACTCAATGTGATTCACTATCTGAAGAGCATTCCTCCAGAG 168807

QY 121 ttgggaagattgtgaaactctagagagactgattgttctgaatctagaatattgag 180
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 Db 168806 CTGGAGAGATTGTG-AAATCTAGAGGAGCTGGATGTCTGGAAATCTGGAATTCACAGAG 168748

QY 181 ctgaccttgtaattgaattgaagaagtagatcatctgtatgatctccacaaag 240
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 Db 168747 CTGCTTTTGAAATTAGTAATTGGAAAGCCAGTTCGATTCGTGATATCTCAGCAACAG 168688

QY 241 ttctccagtlgtcccaatctgtctcgtcgtatgtcgaatttgcagtggttgatatacagc 300
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 Db 168687 TTTTCAGATGTCGCCAGTGTGTCTCTGAGAGATGC-TATTTCCAGTGTGATATCAGC 168629

QY 301 agcaataacctgaccgacctgcgcaagataatagacagctagagagctcgaagcttt 360
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 Db 168638 AACAAATACCTGACTGCTGGCGCAAGAT---ACAGCTGAGAGAGCCCGAGGCTTT 168573

QY 361 ctctgtataaanaaagttgaccactctccatctccatctgacatctgaactgaagaagctc 420
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 Db 168572 CTCCTGTATAGAGCAATTGACCTTCTTACCCCATCTTAACCTGAAGAGCGC 168513

QY 421 acctgttagtcgtcagtgaggaccattgtgtgagactcccaactgcctctgtgactca 480
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 Db 168512 ACCTGTTAGTCGTCAATGGGAGCACCTGGGAGCTTTGAGCTTGTGTGACTCC 168453

QY 481 tccaaccttaaaattgtgaagcttatgacaatcc 518
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 Db 168452 TCCACACCTTTAAATTTGTAAAGCCTTATTAACAATCC 168415

RESULT 5
 HSA310996/c HSA310996 145795 bp DNA HTG 18-APR-2001
 LOCUS Homo sapiens chromosome 3 clone RP6-91P17 map 3p21.3, ***
 DEFINITION SEQUENCING IN PROGRESS ***, 42 ordered pieces.
 ACCESSION AJ310996
 VERSION AJ310996.1 GI:13751170
 KEYWORDS HTG; HTGS_PHASE2.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 145795)
 AUTHORS Kiss,H., Yang,Y., Kost-Altmanova,M., Szeles,A., Kholodnyuk,I.,
 Keira,D., Kiss,C., Klein,G., Imreh,S. and Dumanski,J.P.
 TITLE Transcriptional map of the common eliminated region 1 on human
 3p21.3
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 145795)
 AUTHORS Kiss,H.

TITLE
 JOURNAL
 COMMENT

Direct Submission
 Submitted (17-APR-2001) Kiss H., Microbiology and Tumorbiology
 Center (MNC), Karolinska Institute, Box 280, Stockholm, S-17177,
 SWEDEN
 The sequencing contigs are in order and the gaps between them are
 represented by 100 n's.

Contig 1: 1-2508 Contig 2: 2609-17434 Contig 3: 17535-21987
 Contig 4: 22088-23066 Contig 5: 23167-28845
 Contig 6: 28946-30840 Contig 7: 30941-37879 Contig 8:
 37980-38928 Contig 9: 39029-40834 Contig 10: 40935-44527 Contig
 11: 44628-48077 Contig 12: 48178-52755 Contig 13: 52856-53293
 Contig 14: 53394-54768 Contig 15: 54869-57895 Contig 16:
 57996-59322 Contig 17: 59423-60159 Contig 18: 60260-61331
 Contig 19: 61332-62928 Contig 20: 63029-63852 Contig 21:
 63953-75555 Contig 22: 75656-77760 Contig 23: 77861-79686
 Contig 24: 79787-80857 Contig 25: 80958-87622 Contig 26:
 87723-89164 Contig 27: 89265-90007 Contig 28: 90108-92035
 Contig 29: 92136-97298 Contig 30: 97399-102032 Contig 31:
 102133-106605 Contig 32: 106706-108263 Contig 33: 108364-110022
 Contig 34: 110123-113747 Contig 35: 113848-125151 Contig 36:
 125252-126026 Contig 37: 126127-129649 Contig 38: 129750-132160
 Contig 39: 132261-133125 Contig 40: 133226-135661 Contig 41:
 135762-142148 Contig 42: 142249-145795.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 42 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

1 2508: contig of 2508 bp in length
 2509 2608: gap of 100 bp
 2609 17434: contig of 14826 bp in length
 17435 17534: gap of 100 bp
 17535 21987: contig of 4453 bp in length
 21988 22087: gap of 100 bp
 22088 23066: contig of 979 bp in length
 23067 23166: gap of 100 bp
 23167 28845: contig of 5679 bp in length
 28846 28945: gap of 100 bp
 28946 30840: contig of 1895 bp in length
 30841 30940: gap of 100 bp
 30941 37879: contig of 6339 bp in length
 37880 37979: gap of 100 bp
 37980 38928: contig of 949 bp in length
 38929 39028: gap of 100 bp
 39028 40834: contig of 1806 bp in length
 40835 40934: gap of 100 bp
 40935 44527: contig of 3593 bp in length
 44528 44627: gap of 100 bp
 44628 48077: contig of 3450 bp in length
 48078 48177: gap of 100 bp
 48178 52755: contig of 4578 bp in length
 52756 52855: gap of 100 bp
 52856 53293: contig of 438 bp in length
 53294 53393: gap of 100 bp
 53394 54768: contig of 1375 bp in length
 54769 54868: gap of 100 bp
 54869 57895: contig of 3027 bp in length
 57896 57995: gap of 100 bp
 57996 59322: contig of 1327 bp in length
 59323 59422: gap of 100 bp
 59423 60159: contig of 737 bp in length
 60160 60259: gap of 100 bp
 60260 61231: contig of 972 bp in length
 61232 61331: gap of 100 bp
 61332 62928: contig of 1597 bp in length
 62929 63028: gap of 100 bp
 63029 63852: contig of 824 bp in length
 63853 63952: gap of 100 bp
 63953 75555: contig of 11603 bp in length

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* 75556 75655: gap of 100 bp
* 75656 77760: contig of 2105 bp in length
* 77761 77860: gap of 100 bp
* 77861 79686: contig of 1826 bp in length
* 79687 79786: gap of 100 bp
* 79787 80857: contig of 1071 bp in length
* 80858 80957: gap of 100 bp
* 80958 87622: contig of 6665 bp in length
* 87623 87722: gap of 100 bp
* 87723 89164: contig of 1442 bp in length
* 89165 89264: gap of 100 bp
* 89265 90007: contig of 743 bp in length
* 90008 90107: gap of 100 bp
* 90108 92035: contig of 1928 bp in length
* 92036 92135: gap of 100 bp
* 92136 97298: contig of 5163 bp in length
* 97299 97398: gap of 100 bp
* 97399 102032: contig of 4634 bp in length
* 102033 102132: gap of 100 bp
* 102133 106605: contig of 4473 bp in length
* 106606 106705: gap of 100 bp
* 106706 108263: contig of 1558 bp in length
* 108264 108363: gap of 100 bp
* 108364 110022: contig of 1659 bp in length
* 110023 110122: gap of 100 bp
* 110123 113747: contig of 3625 bp in length
* 113748 113847: gap of 100 bp
* 113848 125151: contig of 11304 bp in length
* 125152 125251: gap of 100 bp
* 125252 126026: contig of 775 bp in length
* 126027 126126: gap of 100 bp
* 126127 129649: contig of 3523 bp in length
* 129650 129749: gap of 100 bp
* 129750 132160: contig of 2411 bp in length
* 132161 132260: gap of 100 bp
* 132261 133125: contig of 865 bp in length
* 133126 133225: gap of 100 bp
* 133226 135661: contig of 2436 bp in length
* 135662 135761: gap of 100 bp
* 135762 142148: contig of 6387 bp in length
* 142149 142248: gap of 100 bp
* 142249 145795: contig of 3547 bp in length.

FEATURES
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            /map="3p21.3"
            /clone="RP6-91P17"

BASE COUNT  39764 a 33207 c 31499 g 37225 t 4100 others

ORIGIN
Query Match      23.6%; Score 161, DB 2; Length 145795;
Best Local Similarity 97.0%; Pred. No. 2e-31;
Matches 164; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 337 aggttagagagcgtgcgagcttctctgtatataaacaagtgtacctaccctccat 396
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Db 61617 AGGCTAAGAGAGCTGCAGAGCTTCTCTGTATATAAACAAGTGTACCTTCCCTAT 61558

QY 397 tccatgtgaacctgaagaagctcaactctgtatagtcagtgaggacattgtgag 456
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Db 61557 TCCATGCTGAACCTGAAGAGAGCTCAGCTGTATACCTGTCACTGGGAGACATTTGCTGAG 61498

QY 457 ctcccaactgcaccttctgtgaactcaaccaccttaaatgtgaagcc 505
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Db 61497 CTCCTCACTGCCTCTTGTGACTCATCCACACCTTTAAGTAGTAGAGCC 61449

RESULT 6
AC068720 AC068720 202324 bp DNA HTG 07-JUL-2000
LOCUS

```

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DEFINITION Homo sapiens chromosome 3 clone RP11-509121, WORKING DRAFT
SEQUENCE 20 unordered pieces.
AC068720
VERSION AC068720.2 GI:8469022
HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 202324)
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 202324)
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 202324)
REFERENCE Waterston, R.H.
          Direct Submission
          Submitted (07-MAY-2000) Genome Sequencing Center, Washington
          University School of Medicine, 4444 Forest Park Parkway, St. Louis,
          MO 63108, USA
COMMENT On Jun 12, 2000 this sequence version replaced gi:7715661.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0509121
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 193150 bases at least Q40
Consensus quality: 195686 bases at least Q30
Consensus quality: 197015 bases at least Q20
Insert size: 200000; agarose-fp
Quality coverage: 4.67 in Q20 bases; agarose-fp
Quality coverage: 4.72 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
-----
1 1576: contig of 1576 bp in length
* 1577 1676: gap of unknown length
* 1677 3263: contig of 1587 bp in length
* 3264 3363: gap of unknown length
* 3364 5443: contig of 2080 bp in length
* 5444 5543: gap of unknown length
* 5544 8196: contig of 2653 bp in length
* 8197 8296: gap of unknown length
* 8297 12038: contig of 3742 bp in length
* 12039 12138: gap of unknown length
* 12139 15992: contig of 3854 bp in length
* 15993 16092: gap of unknown length
* 16093 21192: contig of 5100 bp in length
* 21193 21292: gap of unknown length
* 21293 24766: contig of 3474 bp in length
* 24767 24866: gap of unknown length
* 24867 30824: contig of 5958 bp in length
* 30825 30924: gap of unknown length
* 30925 37154: contig of 6229 bp in length
* 37154 37253: gap of unknown length
* 37254 45262: contig of 8009 bp in length
* 45263 45362: gap of unknown length
* 45363 56733: contig of 11371 bp in length
* 56734 56833: gap of unknown length

```

* 56834 72156: contig of 15323 bp in length
* 72157 72256: gap of unknown length
* 72257 84702: contig of 12446 bp in length
* 84703 84802: gap of unknown length
* 84803 101052: contig of 16250 bp in length
* 101053 101152: gap of unknown length
* 101153 117709: contig of 16557 bp in length
* 117710 117809: gap of unknown length
* 117810 132650: contig of 14841 bp in length
* 132651 132751: gap of unknown length
* 132751 152071: contig of 19321 bp in length
* 152072 152171: gap of unknown length
* 152172 176190: contig of 24019 bp in length
* 176191 176291: gap of unknown length
* 176291 202324: contig of 26034 bp in length.
* Location/Qualifiers
* 1..202324
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="3"
* /clone="RP11-509121"
* 1..1576

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/note="assembly_name:Contig5"
3364..5443
misc_feature /note="assembly_name:Contig6"
5544..8196
misc_feature /note="assembly_name:Contig7"
8297..12038
misc_feature /note="assembly_name:Contig8"
12139..15992
misc_feature /note="assembly_name:Contig9
clone_end:T7
vector_side:right"
16093..21192
misc_feature /note="assembly_name:Contig10"
21293..24766
misc_feature /note="assembly_name:Contig11"
24867..30824
misc_feature /note="assembly_name:Contig12"
30925..37153
misc_feature /note="assembly_name:Contig13"
37254..45262
misc_feature /note="assembly_name:Contig14"
45363..56733
misc_feature /note="assembly_name:Contig15"
56834..72156
misc_feature /note="assembly_name:Contig16"
72257..84702
misc_feature /note="assembly_name:Contig17"
84803..101052
misc_feature /note="assembly_name:Contig18"
101153..117709
misc_feature /note="assembly_name:Contig19"
117810..132650
/note="assembly_name:Contig20
clone_end:SP6
vector_side:left"
132751..152071
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152172..176190
misc_feature /note="assembly_name:Contig22"
176291..202324
misc_feature /note="assembly_name:Contig23"
176291..202324

BASE COUNT 56787 a 45300 c 43765 g 54528 t 1944 others
ORIGIN
Query Match 23.6%; Score 161; DB 2; Length 202324;
Best Local Similarity 97.0%; Pred. No. 2,1e-31;
Matches 164; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 337 aggcctagaggagctgcagagcttctctgtatataaaacaggttgacctacttccctat 396
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Db 96876 AGGCTATGAGGAGGAGCTGCACAGCTTTCTCTGTATATAAAACAGTTACCTACTTCCCTAT 96935
|||||
Oy 397 tccatcgtgaacctaaagaactcactctgtatagtcgctcagtgaggaccattgttgag 456
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Db 96936 TCCTATGCTGAACCTGAACAGCTCTCCTGTAGTCGTCATGGGACCATTTGTGTGAG 96995
|||||
Oy 457 ctcccgaactgcctctgtgactatccacaccttaaatgtglaagcc 505
|||||
Db 96996 CTCCTCACTGCCTTTGTGACTCATTCACACTTTAAAGTGAGTGGCC 97044
|||||

RESULT 7
AC068720/c DNA HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 3 clone RP11-509121, WORKING DRAFT
DEFINITION
SEQUENCE, 20 unordered pieces.
ACCESSION
AC068720.2 GI:8469022
VERSION
AC068720.2
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 202324)
Waterston,R.H.
TITLE
The sequence of Homo sapiens clone
JOURNAL
Unpublished
2 (bases 1 to 202324)
REFERENCE
Waterston,R.H.
AUTHORS
Direct Submission
TITLE
Submitted (07-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
JOURNAL
On Jun 12, 2000 this sequence version replaced gi:7715661.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0509121
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 193150 bases at least Q40
Consensus quality: 195686 bases at least Q30
Consensus quality: 197015 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 200424; sum-of-contigs
Quality coverage: 4.67 in Q20 bases; agarose-fp
Quality coverage: 4.72 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1576: contig of 1576 bp in length
* 1577 1677: gap of unknown length
* 1677 3263: contig of 1587 bp in length
* 3263 3264: gap of unknown length
* 3264 3363: gap of unknown length
* 3363 3364: contig of 2080 bp in length
* 3364 5443: gap of unknown length
* 5443 5444: gap of unknown length
* 5444 8196: contig of 2653 bp in length
* 8196 8296: gap of unknown length

*	8297	12038:	contig of 3742 bp in length
*	12039	12138:	gap of unknown length
*	12139	15992:	contig of 3854 bp in length
*	15993	16092:	gap of unknown length
*	16093	21192:	contig of 5100 bp in length
*	21193	21292:	gap of unknown length
*	21293	24766:	contig of 3474 bp in length
*	24767	24866:	gap of unknown length
*	24867	30824:	contig of 5958 bp in length
*	30825	30924:	gap of unknown length
*	30925	37153:	contig of 6229 bp in length
*	37154	37253:	gap of unknown length
*	37254	45262:	contig of 8009 bp in length
*	45263	45362:	gap of unknown length
*	45363	56733:	contig of 11371 bp in length
*	56734	56833:	gap of unknown length
*	56834	72135:	contig of 15323 bp in length
*	72135	72235:	gap of unknown length
*	72235	84702:	contig of 12446 bp in length
*	84702	84802:	gap of unknown length
*	84803	101052:	contig of 16250 bp in length
*	101053	101152:	gap of unknown length
*	101153	117709:	contig of 16537 bp in length
*	117710	117809:	gap of unknown length
*	117810	132550:	contig of 14841 bp in length
*	132551	132750:	gap of unknown length
*	132751	152071:	contig of 19321 bp in length
*	152072	152171:	gap of unknown length
*	152172	176190:	contig of 24019 bp in length
*	176191	176290:	gap of unknown length
*	176291	202324:	contig of 26034 bp in length

FEATURES

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                   /note="assembly_name:Contig4"
misc_feature      1677. 3263
                   /note="assembly_name:Contig5"
misc_feature      3364. 5443
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misc_feature      5544. 8196
                   /note="assembly_name:Contig7"
misc_feature      8297. 12038
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misc_feature      12139. 15992
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                   vector.side:right"
misc_feature      16093. 21192
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misc_feature      21293. 24766
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misc_feature      45363. 56733
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misc_feature      56834. 72156
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misc_feature      101153. 117709
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misc_feature      clone_end:sp6
                  vector_side:left
132751. .152071
/note="assembly_name:Config1"
misc_feature      152172. .176190
/note="assembly_name:Config2"
misc_feature      176291. .202324
/note="assembly_name:Config3"
BASE COUNT      56787 a 45300 c 43765 g 54528 t 1944 others
ORIGIN

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Query Match	20.2%;	Score 137.8;	DB 2;	Length 202324;
Best Local Similarity	92.4%;	Pred. No. 2.5e-25;		
Matches 145;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;

Db 83500 AGATTGTAGCCTTATGACATCCATTGTATATGCCCATGTGAAGATGGCAATGAA 834

Db 83440 ATAAATGGAAGTGAACGGGATCCGCAACATTTTTCATTAAGCAAGTTAAGAAGCCATATATT 83381

Db 83380 GAAGACCTTAAGAAAGAGGTGGTTACTCATATTTA 83344

RESULT	8
AK021919	
LOCUS	AK021919 2056 bp mRNA PRI 29-SEP-2000
DEFINITION	Homo sapiens cDNA FLJ11857 fis, clone HEMBA1006807, moderately similar to Homo sapiens mRNA for SHOP.

VERSION AK021919.1 GI:10433216
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to

ORGANISM

REFERENCE	1 (sites)
AUTHORS	Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Isogai, T.,

Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nawahari, K., Masuko, Y. and Oshima, A.

REFERENCE	2 (bases 1 to 2056)
AUTHORS	Isogai, T. and Otsuki, T.

Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp).

International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library

etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES	Location/Qualifiers
source	1. . 2056

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/organism="Homo sapiens"
/bb_xref="taxon:9606"
/clone_id="HEMBA1006807"
/clone_lib="HEMBA1"
/dev_stage="embryo, 10 weeks"
/tissue_type="whole embryo, mainly head"
/notes="cloning vector: PME185FL3"

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Query Match	Best Local Similarity	Score	DB	Length
Matches 219; Conservative	47.28;	60.8;	DB 9;	1658;
	0;	Mismatches 242;	Indels 3;	Gaps 1;
QY	10	ctgagctctgcaaaaacaaatctccacatctcagcagaagaatcgyttgttgaagaac	69	
Db	466	CTGGAGCTGAGAGAGAACTCTTACATATCTTCCTGACTCTTACCCAGCTCGAGAGA	525	
QY	70	ctgaagaagacatactgltggttcaactatcgaagaagcattccccaagtgtggagat	129	
Db	526	CTAGAGAACTTGATTGATTAAGAAACATGAAATATATATTGGCCAGATCAATTGGAGCC	585	
QY	130	tgtgaatactcagaagagacttgatctgttcggaatctagaatctaatgagagctccctt	189	
Db	586	CTCTTACATCTTAAAGAAAGATCTCTGGTGGATGGAATC---AACGTGAGAAATTCCTCAG	642	
QY	190	gaattaagtaatttgaagaagcaggttaccattgttagatatcagcaagaatttccagt	249	
Db	643	GAAATAGGAAATCTGAGAACACTCTGTGTTAGATGCTCTTGAAACAGAGTTGGAAGA	702	
QY	250	gtcccaatctgtgtcctgcygagtgcgaattgcagtgagtgatatacagcaataac	309	
Db	703	CTTCCTGAGAAATCAGTGGCCCTGACTTCAATTAACGAGATTAATGATTCCTCCAGACATTA	762	
QY	310	ctgacgcagccgcgcgaagatatagacaggtctagaagagctgcagagcttctctgtat	369	
Db	763	TTAGAAACGATTCGGAGTGGCATTTGAAAACTAAAGAACTGTCATCTTGAAAGTGGAT	822	
QY	370	aaaaaagcttgactactcctccattccatctcgaatccgaagaagcctcactctta	429	
Db	823	CAGAAATGACACTCACACAGATTGCTCGAAGCAGTTGGGCAATGTGAAAGCTCTCAGATTA	882	
QY	430	gtcgcagtgaggacatttggltgagagctcccaactgcccctt	473	
Db	883	GTTCTTACAGAAATTCAGCTCTGACCTGCTGCTAAAGCAATGG	926	
RESULT	10			
LOCUS	BC003193	2156 bp	mRNA	12-JUL-2001
DEFINITION			Homo sapiens, similar to scribbled, clone MGC:936 IMAGE:3504090,	
ACCESSION	BC003193		mRNA, complete cds.	
VERSION	BC003193.1	GI:13112034		
KEYWORDS	MGC.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 2156)			
JOURNAL	Strausberg, R.			
	Direct Submission			
	Submitted (13-FEB-2001) National Institutes of Health, Mammalian			
	Gene Collection (MGC), Cancer Genomics Office, National Cancer			
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
	USA			
	NIH-MGC Project URL: http://mgc.nci.nih.gov			
REMARK	Contact: MGC help desk			
COMMENT	Email: gcgaps-remail.nih.gov			
	Tissue Procurement: ATCC			

[illegible]

RESULT	12
AC027653/c	
LOCUS	AC027653 216481 bp DNA
DEFINITION	Mus musculus chromosome 5 clone RP23-166J14 strain C57BL6/J, 19-SEP-2000
ACCESSION	AC027653
VERSION	AC027653.2 GI:10190772
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	house mouse.
ORGANISM	Mus musculus

```

Db 148604  TAACTATTTCOCATGGGGTGTGTGCTTGCATCACTGACACTTGAGATTATNG 148545
OY 302  gcaataaccctgacccgacctgcgcgaagatatagacagctcagagagctgcagacttc 361
Db 148544  GAAATTAATTATTTTCAGAAATCCCTGTGACACATGTCGTTAGTACAGCAGCTGCTTCAATTAG 148485
OY 362  tctgtataaaaacaagctgacctaccctcc 392
Db 148484  AGTTGAATTAAGAAACAACCTCACCGCTATTTC 148454

RESULT 13
AC079990/c
LOCUS AC079990 133841 bp DNA HTG 21-SEP-2000
DEFINITION Rattus norvegicus chromosome 4 clone Rp31-327J16 strain Brown
ACCESSION AC079990
VERSION AC079990.1 GI:10242411
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 133841)
Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Dietrich,N.L., Gupta,J., Ho,S.-L., Idol,J.,
Lee,I.H.,S.-O., Legaspi,R., Lim,M., Maduro,O.L., Maduro,Y.B.,
Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B.,
Stantilpop,S., Thomas,J.W., Thomas,P.J., Tongson,E.E.,
Touchman,J.W., Tran,J.T., Vogt,J.L., Walker,M.A., Wetherby,K.D. and
Green,E.D.
NISC Mouse Sequencing Initiative
Unpublished
2 (bases 1 to 133841)
Green,E.D.
Direct Submission
Submitted (21-SEP-2000) NIH Intramural Sequencing Center, 8717
Groveomont Circle, Gaithersburg, MD 20877, USA
-----
COMMENT Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
-----
Project Information
Center project name: rc
Center clone name: 327J16
-----
Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 132021 bases at least Q40
Consensus quality: 132388 bases at least Q30
Consensus quality: 132461 bases at least Q20
Insert size: 148000; agarose-fp
Insert size: 197000; pulse-field-gel
Insert size: 133441; sum-of-contrigs
Quality coverage: 9.91x in Q20 bases; agarose-fp
Quality coverage: 7.44x in Q20 bases; pulse-field-gel
Quality coverage: 10.99x in Q20 bases; sum-of-contrigs
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NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1 8955: contrig of 8955 bp in length
* 8956 9055: gap of unknown length
* 9056 17867: contrig of 8812 bp in length

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[illegible]

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SOURCE          Norway rat.
ORGANISM        Rattus norvegicus
REFERENCE       Eukaryote: Metazoa; Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
                1 (bases 1 to 188150)
                Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
                Bouffard,G.G., Dietrich,N.L., Eagle,W.O., Gupta,J., Ho,S.-L.,
                Idol,J., Lee-Lin,S.-Q., Legaspi,R., Lim,M., Maduro,O.L.,
                Maduro,V.B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
                Pearson,R., Staturipop,S., Summers,T.J., Thomas,J.W., Thomas,P.J.,
                Tlionson,E.E., Touchman,J.W., Tran,J.T., Vogt,J.L., Walker,M.A.,
                Wetherby,K.D. and Green,E.D.
                NISC Mouse Sequencing Initiative
TITLE           Unpublished
JOURNAL         2 (bases 1 to 188150)
REFERENCE       Green,E.D.
AUTHORS         Direct Submission
                Submitted (30-AUG-2000) NIH Intramural Sequencing Center, 8717
                Government Circle, Gaithersburg, MD 20877, USA
COMMENT         ----- Genome Center
                Center: NIH Intramural Sequencing Center
                Center code: NISC
                Web site: http://www.nisc.nih.gov
                Contact: nisc.mouse@hprf.nih.gov
                ----- Project Information
                -----
                Center project name: rb
                Center clone name: 0071L1
                ----- Summary Statistics
                Sequencing vector: plasmid; n/a; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.990319
                Consensus quality: 186393 bases at least Q40
                Consensus quality: 187093 bases at least Q30
                Consensus quality: 187475 bases at least Q20
                Insert size: 158000; agarose-1p
                Insert size: 171000; pulse-field-gel
                Quality coverage: 10.16x in Q20 bases; agarose-1p
                Quality coverage: 9.38x in Q20 bases; pulse-field-gel
                Quality coverage: 8.54x in Q20 bases; sum-of-coverage
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                * NOTE: This is a 'working draft' sequence. It currently
                * consists of 4 contigs. The true order of the pieces
                * is not known and their order in this sequence record is
                * arbitrary. Gaps between the contigs are represented as
                * runs of N, but the exact sizes of the gaps are unknown.
                * This record will be updated with the finished sequence
                * as soon as it is available and the accession number will
                * be preserved.
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                * 1 23058: contig of 23058 bp in length
                * 23059 23158: gap of unknown length
                * 23159 65227: contig of 42069 bp in length
                * 65228 65327: gap of unknown length
                * 65328 92131: contig of 26804 bp in length
                * 92132 92231: gap of unknown length
                * 92232 188150: contig of 95919 bp in length.
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                * 1. 188150
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                /strain="Brown Norway"
                /db_xref="taxon:101116"
                /chromosome="4"
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                /clone_11b="RP31"
                1. 23058
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                vector_side:right"
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                /note="assembly_fragment"
                65328. 92131
                /note="assembly_fragment

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[illegible]

Pediatrics-Hematology & Oncology, Texas Children's REIGIN Center
102514, Houston, Texas 77030, USA. Telephone: 713-770-4583
margolinebcm.tmc.edu.

FEATURES

Location/Qualifiers
source 1. .1127

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CDABP0083"
/clone.lib="constructed by Y.T.M. Tsang"

/note="From patient with acute lymphoblastic leukemia;
similar to Homo sapiens cDNA FLJ10470 fis, clone
NT2RP2000032 with GenBank Accession Number AK01332.1"

BASE COUNT 370 a 215 c 214 g 328 t
ORIGIN

Query Match 8.4%; Score 57.4; DB 9; Length 1127;
Best Local Similarity 47.0%; Pred. No. 0.00015;
Matches 178; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 182 tgccttgaattaagtaattgaagcaagttacattgtagatatctcagaacaagt 241
DB 343 TACCAGTGGCAGTATTGATTACGAACTCAGATGCTTAGATGAGCTACACACA 402
QY 242 ttccagtgcccaatctgtcctgcgagatgtcgaattgcagtggttgatatacga 301
DB 403 TTTCATGATTCCTCAATGAAATAGGATTGCTTCAGAACTGCAGCATTTGCATATC 462
QY 302 gcaataacctgaccgacctgcgcgaagataagacaagctagaagagctgcagaagcttc 361
DB 463 GGAACAAGTGGACATCTGCACAAACATTTGTTAAATGCATTAAGTGAAGTGA 522
QY 362 tcttgtataaaacaagttaccacttccctatccatgctgaactgaagaagctca 421
DB 523 ATCTGGACAGAACTGCATCACTCACTCCAGAGAAAGTTGTCAGCTCTCCAGCTCA 582
QY 422 ctctgttagtcgtagtggaacatttggtagagctcccaactgccttgtgaactcat 481
DB 583 CTCAGCTGAGAGTGAAGGAACTGCTTGGACCGCTGCCAGCCAGCTGGGCCAGTGTG 642
QY 482 ccaacaccttaaaattgttaagcctatgagacaatcctatgataatgcccgaatgtgaag 541
DB 643 GGATGCTCAAGAAAGCGGCTTGTTGTGGAAGATCACCTTTTGATATCCCTGCCACTCG 702
QY 542 atggcaatgaataatgga 560
DB 703 AAGTCAAGAGAGCATTTGAA 721

Search completed: February 26, 2002, 10:56:31
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